

SEQUENCE LISTING

<110> Horton, Holly  
Parker, Suezanne  
Manthorpe, Marston  
Felgner, Philip

<120> Treatment of Cancer Using Cytokine-Expressing  
Polynucleotides and Compositions Therefor

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<151> 1997-11-20

<150> US 60/079,914

<151> 1998-03-30

<150> US 60/100,820

<151> 1998-09-15

<150> US 09/196,313

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<170> PatentIn Ver. 2.0

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attgtctcat gagcggatac atatttgaat gtatttagaa aaataaacia ataggggttc 5160  
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<211> 585  
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<220>  
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<220>  
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<222> (70)..(585)

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-20 -15 -10

agc cct gtt gga tct ctg ggc tgt gat ctg cct cag aac cat ggc cta 96  
Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu  
-5 -1 1 5

ctt agc agg aac acc ttg gtg ctt ctg cac caa atg agg aga atc tcc 144  
Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser  
10 15 20 25

cct ttc ttg tgt ctc aag gac aga aga gac ttc agg ttc ccc cag gag 192  
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu  
30 35 40

atg gta aaa ggg agc cag ttg cag aag gcc cat gtc atg tct gtc ctc 240  
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu  
45 50 55

cat gag atg ctg cag cag atc ttc agc ctc ttc cac aca gag cgc tcc 288  
His Glu Met Leu Gln Gln Ile Phe Ser Leu Phe His Thr Glu Arg Ser

60	65	70	
tct gct gcc tgg aac atg acc ctc cta gac caa ctc cac act gga ctt			336
Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu			
75	80	85	
cat cag caa ctg caa cac ctg gag acc tgc ttg ctg cag gta gtg gga			384
His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly			
90	95	100	105
gaa gga gaa tct gct ggg gca att agc agc cct gca ctg acc ttg agg			432
Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg			
110	115	120	
agg tac ttc cag gga atc cgt gtc tac ctg aaa gag aag aaa tac agc			480
Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser			
125	130	135	
gac tgt gcc tgg gaa gtt gtc aga atg gaa atc atg aaa tcc ttg ttc			528
Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe			
140	145	150	
tta tca aca aac atg caa gaa aga ctg aga agt aaa gat aga gac ctg			576
Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu			
155	160	165	
ggc tca tct			585
Gly Ser Ser			
170			
<210> 8			
<211> 195			
<212> PRT			
<213> Homo sapiens			
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Ser Pro Val Gly Ser Leu Gly Cys Asp Leu Pro Gln Asn His Gly Leu			
-5	-1 1	5	
Leu Ser Arg Asn Thr Leu Val Leu Leu His Gln Met Arg Arg Ile Ser			
10	15	20	25
Pro Phe Leu Cys Leu Lys Asp Arg Arg Asp Phe Arg Phe Pro Gln Glu			
30	35	40	
Met Val Lys Gly Ser Gln Leu Gln Lys Ala His Val Met Ser Val Leu			
45	50	55	



Ser Ala Ala Trp Asn Met Thr Leu Leu Asp Gln Leu His Thr Gly Leu  
75 80 85

His Gln Gln Leu Gln His Leu Glu Thr Cys Leu Leu Gln Val Val Gly  
90 95 100 105

Glu Gly Glu Ser Ala Gly Ala Ile Ser Ser Pro Ala Leu Thr Leu Arg  
110 115 120

Arg Tyr Phe Gln Gly Ile Arg Val Tyr Leu Lys Glu Lys Lys Tyr Ser  
125 130 135

Asp Cys Ala Trp Glu Val Val Arg Met Glu Ile Met Lys Ser Leu Phe  
140 145 150

Leu Ser Thr Asn Met Gln Glu Arg Leu Arg Ser Lys Asp Arg Asp Leu  
155 160 165

Gly Ser Ser  
170

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<210> 9
<211> 567
<212> DNA
<213> Homo sapiens
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<220>  
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<400> 9
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Met Ala Ser Pro Phe Ala Leu Leu Met Val Leu Val Val Leu Ser Cys
          -20                -15                      -10
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aag tca agc tgc tct ctg ggc tgt gat ctc cct gag acc cac agc ctg 96  
Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Glu Thr His Ser Leu  
-5 -1 1 5

gat aac agg agg acc ttg atg ctc ctg gca caa atg agc aga atc tct 144

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<210> 10
<211> 189
<212> PRT
<213> Homo sapiens

<400> 10
Met Ala Ser Pro Phe Ala Leu Leu Met Val Leu Val Val Leu Ser Cys
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Lys Ser Ser Cys Ser Leu Gly Cys Asp Leu Pro Glu Thr His Ser Leu
      -5                -1    1                      5
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-27-

Asp Asn Arg Arg Thr Leu Met Leu Leu Ala Gln Met Ser Arg Ile Ser  
10 15 20 25

Pro Ser Ser Cys Leu Met Asp Arg His Asp Phe Gly Phe Pro Gln Glu  
30 35 40

Glu Phe Asp Gly Asn Gln Phe Gln Lys Ala Pro Ala Ile Ser Val Leu  
45 50 55

His Glu Leu Ile Gln Gln Ile Phe Asn Leu Phe Thr Thr Lys Asp Ser  
60 65 70

Ser Ala Ala Trp Asp Glu Asp Leu Leu Asp Lys Phe Cys Thr Glu Leu  
75 80 85

Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Met Gln Glu Glu Arg  
90 95 100 105

Val Gly Glu Thr Pro Leu Met Asn Ala Asp Ser Ile Leu Ala Val Lys  
110 115 120

Lys Tyr Phe Arg Arg Ile Thr Leu Tyr Leu Thr Glu Lys Lys Tyr Ser  
125 130 135

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg Ser Leu Ser  
140 145 150

Leu Ser Thr Asn Leu Gln Glu Arg Leu Arg Arg Lys Glu  
155 160 165

<210> 11  
<211> 567  
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<220>  
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<222> (1)..(567)

<220>  
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<400> 11  
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Met Ala Arg Leu Cys Ala Phe Leu Met Val Leu Ala Val Met Ser Tyr  
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tg	g	cca	acc	tgc	tct	cta	gga	tgt	gac	ctg	cct	cag	act	cat	aac	ctc	96
Trp	Pro	Thr	Cys	Ser	Leu	Gly	Cys	Asp	Leu	Pro	Gln	Thr	His	Asn	Leu		
		-5				-1	1				5						
agg	aac	aag	aga	gcc	ttg	aca	ctc	ctg	gta	caa	atg	agg	aga	ctc	tcc		144
Arg	Asn	Lys	Arg	Ala	Leu	Thr	Leu	Leu	Val	Gln	Met	Arg	Arg	Leu	Ser		
10					15					20					25		
cct	ctc	tcc	tgc	ctg	aag	gac	agg	aag	gac	ttt	gga	ttc	ccg	cag	gag		192
Pro	Leu	Ser	Cys	Leu	Lys	Asp	Arg	Lys	Asp	Phe	Gly	Phe	Pro	Gln	Glu		
				30					35						40		
aag	gtg	gat	gcc	cag	cag	atc	aag	aag	gct	caa	gcc	atc	cct	gtc	ctg		240
Lys	Val	Asp	Ala	Gln	Gln	Ile	Lys	Lys	Ala	Gln	Ala	Ile	Pro	Val	Leu		
			45					50					55				
agt	gag	ctg	acc	cag	cag	atc	ctg	aac	atc	ttc	aca	tca	aag	gac	tca		288
Ser	Glu	Leu	Thr	Gln	Gln	Ile	Leu	Asn	Ile	Phe	Thr	Ser	Lys	Asp	Ser		
		60					65					70					
tct	gct	gct	tgg	aat	gca	acc	ctc	cta	gac	tca	ttc	tgc	aat	gac	ctc		336
Ser	Ala	Ala	Trp	Asn	Ala	Thr	Leu	Leu	Asp	Ser	Phe	Cys	Asn	Asp	Leu		
	75					80					85						
cac	cag	cag	ctc	aat	gac	ctg	caa	ggt	tgt	ctg	atg	cag	cag	gtg	ggg		384
His	Gln	Gln	Leu	Asn	Asp	Leu	Gln	Gly	Cys	Leu	Met	Gln	Gln	Val	Gly		
90					95					100					105		
gtg	cag	gaa	ttt	ccc	ctg	acc	cag	gaa	gat	gcc	ctg	ctg	gct	gtg	agg		432
Val	Gln	Glu	Phe	Pro	Leu	Thr	Gln	Glu	Asp	Ala	Leu	Leu	Ala	Val	Arg		
				110					115					120			
aaa	tac	ttc	cac	agg	atc	act	gtg	tac	ctg	aga	gag	aag	aaa	cac	agc		480
Lys	Tyr	Phe	His	Arg	Ile	Thr	Val	Tyr	Leu	Arg	Glu	Lys	Lys	His	Ser		
			125					130					135				
ccc	tgt	gcc	tgg	gag	gtg	gtc	aga	gca	gaa	gtc	tgg	aga	gcc	ctg	tct		528
Pro	Cys	Ala	Trp	Glu	Val	Val	Arg	Ala	Glu	Val	Trp	Arg	Ala	Leu	Ser		
		140					145					150					
tcc	tct	gcc	aat	gtg	ctg	gga	aga	ctg	aga	gaa	gag	aaa					567
Ser	Ser	Ala	Asn	Val	Leu	Gly	Arg	Leu	Arg	Glu	Glu	Lys					
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 <211> 189  
 <212> PRT  
 <213> Mus musculus

<400> 12

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Trp Pro Thr Cys Ser Leu Gly Cys Asp Leu Pro Gln Thr His Asn Leu  
-5 -1 1 5

Arg Asn Lys Arg Ala Leu Thr Leu Leu Val Gln Met Arg Arg Leu Ser  
10 15 20 25

Pro Leu Ser Cys Leu Lys Asp Arg Lys Asp Phe Gly Phe Pro Gln Glu  
30 35 40

Lys Val Asp Ala Gln Gln Ile Lys Lys Ala Gln Ala Ile Pro Val Leu  
45 50 55

Ser Glu Leu Thr Gln Gln Ile Leu Asn Ile Phe Thr Ser Lys Asp Ser  
60 65 70

Ser Ala Ala Trp Asn Ala Thr Leu Leu Asp Ser Phe Cys Asn Asp Leu  
75 80 85

His Gln Gln Leu Asn Asp Leu Gln Gly Cys Leu Met Gln Gln Val Gly  
90 95 100 105

Val Gln Glu Phe Pro Leu Thr Gln Glu Asp Ala Leu Leu Ala Val Arg  
110 115 120

Lys Tyr Phe His Arg Ile Thr Val Tyr Leu Arg Glu Lys Lys His Ser  
125 130 135

Pro Cys Ala Trp Glu Val Val Arg Ala Glu Val Trp Arg Ala Leu Ser  
140 145 150

Ser Ser Ala Asn Val Leu Gly Arg Leu Arg Glu Glu Lys  
155 160 165

<210> 13  
<211> 459  
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<222> (1)..(459)

<220>  
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<220>  
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<400> 13

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gtc aca aac agt gca cct act tca agt tct aca aag aaa aca cag cta	96
Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys Lys Thr Gln Leu	
-1 1 5 10	
caa ctg gag cat tta ctt ctg gat tta cag atg att ttg aat gga att	144
Gln Leu Glu His Leu Leu Leu Asp Leu Gln Met Ile Leu Asn Gly Ile	
15 20 25	
aat aat tac aag aat ccc aaa ctc acc agg atg ctc aca ttt aag ttt	192
Asn Asn Tyr Lys Asn Pro Lys Leu Thr Arg Met Leu Thr Phe Lys Phe	
30 35 40	
tac atg ccc aag aag gcc aca gaa ctg aaa cat ctt cag tgt cta gaa	240
Tyr Met Pro Lys Lys Ala Thr Glu Leu Lys His Leu Gln Cys Leu Glu	
45 50 55 60	
gaa gaa ctc aaa cct ctg gag gaa gtg cta aat tta gct caa agc aaa	288
Glu Glu Leu Lys Pro Leu Glu Glu Val Leu Asn Leu Ala Gln Ser Lys	
65 70 75	
aac ttt cac tta aga ccc agg gac tta atc agc aat atc aac gta ata	336
Asn Phe His Leu Arg Pro Arg Asp Leu Ile Ser Asn Ile Asn Val Ile	
80 85 90	
gtt ctg gaa cta aag gga tct gaa aca aca ttc atg tgt gaa tat gct	384
Val Leu Glu Leu Lys Gly Ser Glu Thr Thr Phe Met Cys Glu Tyr Ala	
95 100 105	
gat gag aca gca acc att gta gaa ttt ctg aac aga tgg att acc ttt	432
Asp Glu Thr Ala Thr Ile Val Glu Phe Leu Asn Arg Trp Ile Thr Phe	
110 115 120	
tgt caa agc atc atc tca aca ctg act	459
Cys Gln Ser Ile Ile Ser Thr Leu Thr	
125 130	

<210> 14

<211> 153

<212> PRT

<213> Homo sapiens

<400> 14

Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu
-20 -15 -10 -5

[illegible]

26

26

<210> 17  
<211> 26  
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<220>  
<223> Description of Artificial Sequence:PCR oligo

<400> 17  
aactgcagat ggcctcgccc ttgct 26

<210> 18  
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<220>  
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<400> 18  
cgggatacctt attccttcct ccttaatc 28

<210> 19  
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<220>  
<223> Description of Artificial Sequence:PCR oligo

<400> 19  
gctctagatg gccctcctgt tccct 25

<210> 20  
<211> 26  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence:PCR oligo

<400> 20  
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<210> 21  
<211> 36  
<212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR oligo

<400> 21

acgcgtcgac atgtgtcctc agaagctaac catctc

36

<210> 22

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR oligo

<400> 22

gcggatccct aggatcggac cctgcaggga acac

34

<210> 23

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR oligo

<400> 23

catgccatgg gtcaatcacg ctacctcctc tttttgg

37

<210> 24

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PCR oligo

<400> 24

gcggatcctc aggcggagct cagatagccc

30

<210> 25

<211> 5469

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1923)..(2393)

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<221> sig\_peptide

<222> (1923)..(1994)

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<221> mat\_peptide

<222> (1995)..(2393)

<400> 25

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